

09397550 seq 20

RESULT 1  
Y92322  
ID Y92322 standard; Protein; 1145 AA.  
XX  
AC Y92322;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Human alpha-2-delta-B calcium channel subunit polypeptide.  
XX  
KW alpha-2-delta-B; calcium channel subunit; 3p21.3; gabapentin; cytostatic;  
KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant.  
XX  
OS Homo sapiens.  
XX  
PN WO200020450-A2.  
XX  
PD 13-APR-2000.  
XX  
PF 07-OCT-1999; 99WO-US23519.  
XX  
PR 07-OCT-1998; 98US-0103322.  
PR 30-OCT-1998; 98US-0106473.  
PR 29-DEC-1998; 98US-0114088.  
XX  
PA (WARN ) WARNER LAMBERT CO.  
XX  
PI Johns MA, Moldover B, Offord JD;  
XX  
DR WPI; 2000-303744/26.  
DR N-PSDB; A09255.  
XX  
PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D  
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,  
PT anxiety, multiple sclerosis or cancer  
XX  
PS Example 1; Page 62-63; 88pp; English.  
XX  
CC The alpha-2-delta-B gene encodes a calcium channel subunit polypeptide.  
CC The gene has been mapped to chromosome 3p21.3. This gene and the related  
CC alpha-2-delta-C and -D genes are useful for protecting mammalian cells  
CC from abnormal calcium flux by introducing expression vectors containing  
CC the respective gene into mammalian cells. The antisense genes are also  
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein  
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.  
CC Therefore, alpha-delta-2 proteins may also be targeted to treat  
CC seizure-related syndromes, migraine, ataxia, vestibular defects, chronic  
CC pain, sleep interference, anxiety, amyotrophic lateral sclerosis (ALS),  
CC multiple sclerosis, mania, tremor, parkinsonism, substance abuse or  
CC addiction syndromes, mood, depression or cancer.  
XX  
SQ Sequence 1145 AA;

Query Match 100.0%; Score 6089; DB 21; Length 1145;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAVPARTCGASRPGPARTARPWPGCGPHPGPGTRRPTSGPPRPLWLLPLPLLAAPGAS	60
Db	1	mavpartcgasrpgpartarpwpgcgphpgpgtrrptsgpprplwllpllllaapgas	60
Qy	61	AYSFPQQHTMQHWARRLEQEVGDGVMRIFGGVQQLREIYKDNRLFEVQENEPQKLVEKVA	120
Db	61	aysfpqqhtmqhwarrleqevdgvmrifggvqqlreiykdnrnlfevqenepqklvekva	120
Qy	121	GDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVER	180
Db	121	gdieslldrkvqalkrladaaenfqkahrwqdnikeedivyydakadaelddpesedver	180
Qy	181	GSKASTLRLDFIEDPNFKNVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRR	240

```

Db 181 gskastlrlldfiedpnfknkvnsyaavqiptdiykgstvilnelnwtealenvfmenrr 240
Qy 241 QDPTLLWQVFGSATGVTRYYPATPWRAPKKIDLYDVRRRPWYIQGASSPKDMVIIVDVSG 300
Db 241 qdptllwqvfgsatgvtryypatpwrapkkidlydvrrrpwyiqgasspkdmviivdvsg 300
Qy 301 SVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPVSCFTHLVQANVRNKKVFKEAV 360
Db 301 svsgltlklmktsvcemldtlsdddyvnvasfnekagpvscfthlvqanvrnkkvfkeav 360
Qy 361 QGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMMIMFTDGGEDRVQDVFEKYNWPNRT 420
Db 361 qgmvakgttgykagfeyafdqlqnsnitrancnkmimftdggedrvqdvfekynwpnrt 420
Qy 421 VRVFTFSVGQHNYDVTPLQWMACANKGYFEIPSIGAIRINTQEYLDVLGRPMVLAGEA 480
Db 421 vrvftfsvgqhnydvtplqwmacankgyfeipsigairintqeyldvlgrpmvlagkea 480
Qy 481 KQVQWTVNYEDALGLGLVVTGTLVPFNLTQDGPGEKKNLILGVMGIDVALNDIKRLTPN 540
Db 481 kqvqwtvnyedalglglvvtgtlpvfnltqdgpggeknqililgvmgidvalndikrltpn 540
Qy 541 YTLGANGYVFAIDLNGYVLLHPNLKPQTTFREPVTLDFLDAELEDENKEEIRSMIDGN 600
Db 541 ytlgangyvfaidlngyvllhpnlpqttnfrepvtldfldaeledenkeeirsmidgn 600
Qy 601 KGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSGLVLPPYSTFYQLANLSDQILQV 660
Db 601 kghkqirtlvkslderyidevtrnytwvpirstnysglvlppystfylqanlsdqilqv 660
Qy 661 KYFEFLLPSSFESEGHVFIAPREYCKDLNASDNNTFLKNFIELMEKVTPDSKQCNNFLL 720
Db 661 kyfefllpssfeseghvfiapreyckdlnasdnnteflknfielmekvtpdskqcnnfll 720
Qy 721 HNLILDGTGITQQLVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNA 780
Db 721 hnildtgtitqqlvervwrddqdlntysllavfaatdggitrvfnpkaedwtenpepfna 780
Qy 781 SFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELS LGRRTLRAVVGVKLD 840
Db 781 sfyrrsldnhgyvfkpphqdallrplelendtvgilvstavelslgrrtlrvavvgvkld 840
Qy 841 LEAWAEKFKVLASNRTHQDQPKCGPNSHCEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQ 900
Db 841 leawaekfkvlasnrtHQDqpkcgpnshcemdcevnnedllcviddggflvlsnqnHQ 900
Qy 901 WDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFPVTVADF 960
Db 901 wdqvgrffsevdanlmlalynnsfytrkesydyqaacapppgnlgaaprgvfvptvadf 960
Qy 961 LNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAGSPETRESSCVMKQTQYYFGSVNA 1020
Db 961 lnlawwtsaaawslfqqlllygliyhswfqadpaeeagspetresscvmkqtqyyfgsvna 1020
Qy 1021 SYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPADGPEQCEL 1080
Db 1021 synaiidcgncsrlfhaqrLtnTnllfvvaeKplcsqceagrllqkethcpadgpeqcel 1080
Qy 1081 VQRPRYRRGPHICFDYNATEDTSDCGRGASFPPSLGVLVSLQLLLLLGLPPRPQPVLVH 1140
Db 1081 vqrpryrrgphicfdynatedtsdcgrgasfppslgvlvslqlllllglpprpqpvlvh 1140
Qy 1141 ASRRL 1145
Db 1141 asrrl 1145

```

RESULT 2  
 R71015  
 ID R71015 standard; Protein; 1084 AA.

XX  
 AC R71015;  
 XX  
 DT 01-DEC-1995 (first entry)  
 XX  
 DE Human neuronal calcium channel subunit alpha 2e.  
 XX  
 KW Calcium channel subunit; antagonist; agonist; diagnosis;  
 KW Lambert Eaton Syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9504822-A.  
 XX  
 PD 16-FEB-1995.  
 XX  
 PF 11-AUG-1994; 94WO-US09230.  
 XX  
 PR 11-AUG-1993; 93US-0105536.  
 PR 05-NOV-1993; 93US-0149097.  
 XX  
 PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 XX  
 PI Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;  
 XX  
 DR WPI; 1995-090900/12.  
 DR N-PSDB; Q84669.  
 XX  
 PT DNA encoding human calcium channel sub-unit(s) - used for  
 PT developing prods. for studying calcium channels, e.g. for  
 PT obtaining agonists and antagonists  
 XX  
 PS Disclosure; Page 248-253; 285pp; English.  
 XX  
 CC Human neuronal alpha 2 coding sequence (Q84664) transcript is  
 CC differentially processed in skeletal muscle, aorta, and CNS in  
 CC the region corresp. to nt 1595-1942 of Q84664 in each of the  
 CC tissues. Five alternatively spliced variant transcripts that differ  
 CC in the presence or absence or one to three different portions of  
 CC this region. There are three sequences involved (see Q84664 FT  
 CC and Q84665 FT), sequence 1, sequence 2 and sequence 3. The five  
 CC alpha 2 encoding transcripts from the different tissues include  
 CC different combinations of the three sequences, except for one of  
 CC the alpha 2 transcripts expressed in aorta which lacks all three  
 CC sequences. The five alpha 2 forms identified are (1) a form that  
 CC lacks sequence 3 called alpha 2a, expressed in skeletal muscle  
 CC (2) one that lacks sequence 1 called alpha 2b, expressed in CNS  
 CC (3) one that lacks sequences 1 and 2 called alpha 2c, expressed in  
 CC aorta (4) one that lacks sequences 1, 2 and 3 called alpha 2d,  
 CC expressed in aorta and (5) one that lacks sequences 1 and 3  
 CC called alpha 2e. The DNA and AA sequences of alpha 2a - alpha 2e  
 CC are set forth in Q84666-Q84669 and R71012-R71015 respectively.  
 XX  
 SQ Sequence 1084 AA;

Query Match 50.2%; Score 3054; DB 16; Length 1084;  
 Best Local Similarity 54.3%; Pred. No. 5.1e-260;  
 Matches 592; Conservative 175; Mismatches 292; Indels 32; Gaps 14;

Qy 44 LWLLLPLLLAAGASAYSFPQOHTMQHWARRLEQEV DGV MRIFGGVQQLREIYKDNRN 103  
 | | | | | : | | | | : : : : : : : | | | : | : :  
 Db 7 laltltlftqsligpsseepfpsavtikswdkmqedlvtlaktasgvnqlvdiyekyqd 66  
 Qy 104 LFEVQENEPQKLVEKVAGDIESLLDRKVQALKRLADAENFQKAHRWQDNIKEEDIVYYD 163  
 | : | : | : | | | | | | : : | | | | | : : : : : : : : : : : : : : :  
 Db 67 lytvepnnaqlveiaardiekllsnrskalvslaleaekvqaahqwredfasnevvyyn 126  
 Qy 164 AKADAELDDPESEDVERGSKASTLRDLFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILN 223  
 | | | | | | | | | : : : | | | | : : : | | | | | | : | : | : | : | : | :  
 Db 127 akddl---dpekndsepgsq--rikpvfiedanfrqisyqhaavhiptdiyegstivln 181



Qy 224 ELNWEALENVFMENRRQDPTLLWQVFGSATGVTRYYPATPW---RAPKKIDLYDVRRR 279  
 Db 182 elnwtasaldevfkknreedpsllwqvfsgsatglaryypaspwvdsrtpnkidlydvrrr 241  
 Qy 280 PWYIQGASSPKDMVIIVDVSGSVSGLTLKLMKTSVCEMLDLSDDDDYVNVASFNEKAQPV 339  
 Db 242 pwyiqgaaspkdmllilvdvsgsvsgltlklirtsvsemletlsdddfvnvasfnsnaqdv 301  
 Qy 340 SCFTHLVQANVRNKKVFKEAVQGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMMMF 399  
 Db 302 scfqhlvqanvrnkklkdavnnitakgitdykkgfsfafeqllnynvsrancnkiimlf 361  
 Qy 400 TDGGEDRVQDVFEKYNWPNRTVRVFTFSVGQHNVDVTPLQWMACANKGYFEIPSIGAIR 459  
 Db 362 tdggeeraqeifnkyn-kdkkvrfrfsvgqhnyergpiqwmacenkgyyeipsigair 420  
 Qy 460 INTQEYLDVLRPMVLAGEAKQVQWNTVYEDALGLGLVVTGTLVPVFNLTQ--DGPGEKK 517  
 Db 421 intqeyldvlgrpmvlagdkakqvqwtvnydalelglvitgtlvpvfnitgqfenktnlk 480  
 Qy 518 NQLILGVMGIDVALNDIKRLTPNYTLGANGYVFAIDLNGYVLLHPNLKPQTTFNREPVT 577  
 Db 481 nqlilgvmgvdvsledikrltprftlcpngyyfaidpnygvllhpnlgpknpksgqepvtl 540  
 Qy 578 DFLDAELEDENKEEIRSMIDGNKGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSL 637  
 Db 541 dflaelendikveirnkmidgesgektfrtlvksqderyidkgnrtytwtpvngtdysl 600  
 Qy 638 GLVLPPYSTFYLOANLSDQILQVKYFEFLPSSFESEGHVFIAPREYCKDLNASDNNTF 697  
 Db 601 alvlpstysfyikakleetitqarysetlkpndfeesgytfiaprdocndlkisdnntef 660  
 Qy 698 LKNFIELMEKVTPDSKQCNNFLLHNLILDTGITQQLVERVWRDQDLNTYSL LAVFAATDG 757  
 Db 661 llnfnfidrktppnpscnadlinrvlldagftnelvqnywskq-nikgvkarfvvtdg 719  
 Qy 758 GITRVFPNKAADWTENPEPFNASFYRRSLDNHGYVFKPPHQDALLRPLELNDTVGILV 817  
 Db 720 gitrvypkeagenwqenpetyedsfykrslndndnyvftapyfnk-sgpgayes---gimv 775  
 Qy 818 STAVELSLGRRTLPAVVGKLDLEAWAEKFKVLASNRTHQDQPQKC-GPNSHCEMDCEV 876  
 Db 776 skaveiyiqgkllkpavvgikidvnswienf-----tktsirdp--cagp---vcdckr 824  
 Qy 877 NNEDLLCVLIDGGFLVLSNQNHQWDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAA 936  
 Db 825 nsdvmdcvilddggfllmanhddytnqigrffgeidpslmrhlvnisvyafnksydyqsv 884  
 Qy 937 CAPQPPGNLGAAPRGVFPVTVADFLNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAE 996  
 Db 885 cepgaapkqgghrsayvpsvadilqigwwataaawsilqqfllsltfprlleavemedd 944  
 Qy 997 G-SPETRESSCVMKQTYFYFGSVNASYNAIDCGNCSRLFHAQRLTNTNLLFVVAEKPLC 1055  
 Db 945 dftaslskqsciteqtqyffdnksksfsgvldcgncsrifhgeklmntnlifimveskgt 1004  
 Qy 1056 SQCEAGRLLQKETHCPADGPEQCELVQRPYRRGPHICFDYNATEDTSDCGRGASFPPSL 1115  
 Db 1005 cpcdtrlliaqeq--tsdgpnpdcmvkqpryrkqpdvcdnnvledytdcggvsglnpsl 1062  
 Qy 1116 GVLVSLQLLLL 1126  
 Db 1063 wyiigiqflll 1073

RESULT 3  
 W63155  
 ID W63155 standard; Protein; 1084 AA.  
 XX  
 AC W63155;

```

XX      12-OCT-1998  (first entry)
XX
DE      Human calcium channel alpha-2e subunit.
XX
KW      Alpha-2 subunit; human; calcium channel; assay; detection;
KW      characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX
OS      Homo sapiens.
XX
PN      US5792846-A.
XX
PD      11-AUG-1998.
XX
PF      31-MAY-1995;    95US-0455543.
XX
PR      04-APR-1994;    94US-0223305.
PR      04-APR-1988;    88US-0176899.
PR      04-APR-1989;    89US-0603751.
PR      04-APR-1989;    89WO-US01408.
PR      20-FEB-1990;    90US-0482384.
PR      30-NOV-1990;    90US-0620250.
PR      15-AUG-1991;    91US-0745206.
PR      31-MAY-1995;    95US-0455543.
XX
PA      (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI      Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
PI      Williams ME;
XX
DR      WPI; 1998-456192/39.
DR      N-PSDB; V42704.
XX
PT      DNA encoding human calcium channel alpha 1B sub:unit protein -
PT      useful for recombinant production of the channel for screening of
PT      its modulators, and diagnosis of Lambert Eaton Syndrome
XX
PS      Claim 3; Columns 305-310; 166pp; English.
XX
CC      The present sequence represents the alpha-2e subunit of a human calcium
CC      channel. Calcium channels are membrane-spanning, multi-subunit proteins
CC      that allow controlled entry of calcium ions into cells. This leads
CC      to depolarisation events required for muscle contraction. The recombinant
CC      subunit, when expressed with nucleic acids encoding the complete calcium
CC      channel, can be used in assays for the detection and characterisation of
CC      compounds that modulate the channel. The DNA encoding the subunits can
CC      be alternatively spliced when transcribed, giving more than one form of
CC      the protein from the same transcript, each having slightly different
CC      properties. In addition, the reactivity of the alpha 1 subunit with IgG
CC      molecules from the serum of an individual with Lambert Eaton Syndrome
CC      (LES) can be used as a diagnostic for the disease.
XX
SQ      Sequence    1084 AA;

Query Match          50.2%;  Score 3054;  DB 19;  Length 1084;
Best Local Similarity 54.3%;  Pred. No. 5.1e-260;
Matches 592;  Conservative 175;  Mismatches 292;  Indels 32;  Gaps 14;

Qy      44  LWLLLP LLP LLAAPGASAYSFPQQHTMQHWRRLQEVDGVMRIFGGVQQLREIYKDNRN 103
Db      7   lal tltl fqslligpsseepfpsavtikswvdkmqedlvtlaktasgvnlvdiyekyqd 66

Qy      104 LFEVQENEPQKLVEKVAGDIESLLDRKVQALKRLADAENFQKAHRWQDNIKEEDIVYYD 163
Db      67  lytvepnнарqlveiaardiekllsnrskalvslaleakvqaahqwredfasnevvyyn 126

Qy      164 AKADAELDDPESEDVERGSKASTLRDLFIEDPNFKKNVNSYAAVQIPTDIYKGSTVILN 223
Db      127 akddl---dpekndsepqsg--rikpvfiedanfgqrqisyqhaavhiptdiyeqstivln 181

```

Qy 224 ELNWTEALENVFMENRRQDPTLLWQVFGSATGVTRYYPATPW----RAPKKIDLYDVRRR 279  
 ||||| ||: || :|| :||:|||||||: ||||:| | | |||||  
 Db 182 elnwtasaldevfkknreedpsllwqvfsgsatglaryypaspwvndsrtpnkidlydvrrr 241

Qy 280 PWYIQGASSPKDMVIIVDVSGSVSGLTLKLMKTSVCEMLDLSDDDYVNVASFNEKAQPV 339  
 |||||:|||||:|:|||||||:||||| |||:|||||:||||| || |  
 Db 242 pwyiqgaaspkdmllilvdvsgsvsgltlklirtsvsemletlsdddfvnvasfnsnaqdv 301

Qy 340 SCFTHLVQANVRNKKVFKEAVQGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMMMF 399  
 ||| ||||| ||||| ||:| | || | || | :||:| | | :||:|||||:|:|  
 Db 302 scfqhlvqanvrnkklkdavnnitakgitdykkgfsfafeqllnynvsrancnkiimlf 361

Qy 400 TDGGEDRVQDVFEKYNWPNRTVRVFTFSVGOHNYDVTPLQWMACANKGYFFEIPSIGAIR 459  
 |||||:| ||:| ||| :| ||| |||||:| :||| |||||:|||||  
 Db 362 tdggeeraqeifnkyn-kdkkvrvfrfsvgqhnyergpiqwmacenkgyyeipsigair 420

Qy 460 INTQEYLDVLGRPMVLAGEAKQVQWTVNYEDALGLGLVVTGTLPVFNLTQ--DGPGEKK 517  
 |||||:|||||:|:||||||| ||| ||||:|||||:| :| |  
 Db 421 intqeyldvlgrpmvlagdkakqvqwtvnyldalelglvitgtlvpfnitgqfenktnlk 480

Qy 518 NQLILGVMGIDVALNDIKRLTPNYTLGANGYVFAIDLNGYVLLHPNLKPQTTNFPVPVL 577  
 |||||:|:| ||||| :|| ||| ||| |||||:| :|||  
 Db 481 nqlilgvmgvdvsledikrltprftlcpngyyfaidpngyvlhpnlgpknpsqepvtl 540

Qy 578 DFLDAELEDENKEEIRRSMDIGNKGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSL 637  
 |||||:| ||| |||| | | |||| |||||: | ||| |: |:  
 Db 541 dflaelendikveirnkmidgesgektfrtlvksqderyidkgnrtywtvpvngtdysl 600

Qy 638 GLVLPPYSTFYQLQANLSDQILQVKYFEFLPSSFESEGHVFIAPREYCKDLNASDNNTF 697  
 |||| || :||:| | :| | | :| | :| ||||:| || |||||  
 Db 601 alvlpfysfyyikakleetitqarysetlkpdnfeesgytffiaprdycndlkisdnntef 660

Qy 698 LKNFIELMEKVTPDSKQCNNFLHNLILDTGITQQLVERVWRDQDLNTYSLAVFAATDG 757  
 || | :||: || ||: || || ||: || | | | :| | |||  
 Db 661 llfnfefdrrktppnpscnadlinrvlldagftnelvqnywskqk-nikgvkarfvvtdg 719

Qy 758 GITRVFPNKAEDWTENPEPFNASFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILV 817  
 |||||:| :| | |||| : |||:|||| ||| |: : | |: ||:  
 Db 720 gitrvvpkeagenwqenpetyedsfykrsldndnyvftapyfnk-sgpgayes---gimv 775

Qy 818 STAVELSLGRRTLRLPAVVGKLDLEAWAEKFKVLASNRTHQDQPKC-GPNSHCEMDCEV 876  
 | ||| : : |:||||:|:| :| | :| | | | ||| ||:  
 Db 776 skaveiyiqgkllkpavvgikidvnswief-----tktsirdp--cagp---vcdckr 824

Qy 877 NNEDLLCVLIDGGFLVLSNQNHQWDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAA 936  
 |: : ||:|||||:| :| :|:|||| |:| :|| | | | :||||:  
 Db 825 nsdvmdcvilddggfllmanhddytnqigrffgeidpslmrhlvnisvyafnksydyqsv 884

Qy 937 CAPQPPGNLGAAPRGVFPVTVADFLNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAE 996  
 || | || | :||:|| | : || :||||: || | : :| | :  
 Db 885 cepgaapkqgaghrsayvpsvadilqigwwataaawsilqqfllsltfprlleavemedd 944

Qy 997 G-SPETRESSCVMKQTQYFSGSVNASYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLC 1055  
 : : ||: ||||:| :| :|: |||||:| || ||||:|:|  
 Db 945 dftaslskqsciteqtqyffndsksfsgvldcgncsrifhgeklmntnlifimveskgt 1004

Qy 1056 SQCEAGRLQLQKETHCPADGPEQCELVQRPRYRRGPHICFDYNATEDTSDCGRGASFPPSL 1115  
 |: |:| | :||| |:|:||||:| |:| | | |:| | : |||  
 Db 1005 cpcdtrlliaeq--tsdgpnpvcdmvkqpryrkqpdvcfdnnvledydcggvsglnpsl 1062

Qy 1116 GVLVSLQLLLL 1126  
 : :| |||  
 Db 1063 wyiigiqflll 1073

RESULT 11  
 R73056  
 ID R73056 standard; Protein; 1106 AA.  
 XX

AC R73056;  
 XX  
 DT 02-NOV-1995 (first entry)  
 XX  
 DE Rabbit skeletal calcium channel (alpha)2-subunit.  
 XX  
 KW Calcium channel; (alpha)2 subunit.  
 XX  
 OS Oryctolagus cuniculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT /label= signal peptide  
 FT Modified-site 94  
 FT /label= potential N-linked glycosylation site  
 FT Modified-site 138  
 FT /label= see above  
 FT Modified-site 186  
 FT /label= see above  
 FT Modified-site 326  
 FT /label= see above  
 FT Modified-site 350  
 FT /label= see above  
 FT Modified-site 470  
 FT /label= see above  
 FT Modified-site 477  
 FT /label= see above  
 FT Modified-site 606  
 FT /label= see above  
 FT Modified-site 615  
 FT /label= see above  
 FT Modified-site 678  
 FT /label= see above  
 FT Modified-site 697  
 FT /label= see above  
 FT Modified-site 784  
 FT /label= see above  
 FT Modified-site 827  
 FT /label= see above  
 FT Modified-site 891  
 FT /label= see above  
 FT Modified-site 914  
 FT /label= see above  
 FT Modified-site 988  
 FT /label= see above  
 FT Modified-site 1081  
 FT /label= see above  
 FT Modified-site 503  
 FT /label= potential cAMP-dependent phosphorylation  
 FT Modified-site 848  
 FT /label= see above  
 FT Region 448..471  
 FT /label= putative transmembrane region  
 FT Region 921..945  
 FT /label= see above  
 FT Region 1082..1101  
 FT /label= see above  
 XX  
 PN US5407820-A.  
 XX  
 PD 18-APR-1995.  
 XX  
 PF 04-APR-1988; 88US-0176899.  
 XX  
 PR 04-APR-1989; 89US-0603751.  
 PR 04-APR-1988; 88US-0176899.  
 PR 13-JUL-1992; 92US-0914231.  
 XX  
 PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 XX  
 PI Brenner R, Ellis SB, Harpold MM, Schwartz A, Williams ME;



```

XX
DR   WPI; 1995-161088/21.
DR   N-PSDB; Q87979.
XX
PT   DNA encoding alpha-1 and alpha-2 calcium channel sub-unit(s) -
PT   for detecting calcium channel agonists/antagonists or
PT   Lambert-Eaton syndrome.
XX
PS   Disclosure; Fig 2; 32pp; English.
XX
CC   The nt sequence in Q87979 was determined from two clones which
CC   overlapped to span the coding sequence of the (alpha)2-subunit.
CC   Five nt differences (see Q87979 FT) among individual clones were
CC   observed resulting in four AA changes. The AAs were finally
CC   determined to be as follows: Asn at residue 57, Lys at residue 116
CC   and a deletion of Ser at residue 620. The deduced AA sequence
CC   (R73056) yields a calculate Mr of 125,018, in contrast to the
CC   observed Mr 165K-175K (under non-reducing conditions; Mr 135K-
CC   175K under reducing conditions) determined previously using SDS
CC   polyacrylamide gel electrophoresis.
XX
SQ   Sequence    1106 AA;

Query Match          49.9%; Score 3040; DB 16; Length 1106;
Best Local Similarity 53.0%; Pred. No. 9.1e-259;
Matches 595; Conservative 183; Mismatches 276; Indels 68; Gaps 20;

Qy   42 RPL-----WLLLPLLLAAPGASAYSFPQQHTMQHWARRLEQEV DGV MRIFGGVQ 92
      |||      ||      :| | :| || | :| | :| :| :| :| :| :|
Db   5 rplawtltlwqawl-----ilgip-sseepfpsavtikswvdkmqedlvtlaktasgvh 57

Qy   93 QLREIYKDNRNLFQENEPQKLVEKVAGDIESLLDRKVQALKRLADAAENFQKAHRWQD 152
      || :||: :||: || :||| | ||| || :|| ||| || | ||:|:
Db   58 qlvdiyekyqdltyvepnarqlveiaardiekllsnrskalvrlaleaekvqaahqwre 117

Qy   153 NIKEEDIVYYDAKADAELDDPESEDVERGSKASTLR LDFIEDPNFKNKVNYSYAAVQIPT 212
      : :|||:| | | || | | ||: :| ||:| ||: :| | :||| |||
Db   118 dfasnevvyynakddl---dpekndsepgsq--rikpvfiddanfrqrqvsyqhaavhipt 172

Qy   213 DIYKGSTVILNELNWTEALENVFMENRRQDPTLLWQVFGSATGVTRYYPATPW----RAP 268
      |||:| |:| |:| ||| ||:| | :| | |:| |:| |:| |:| |:| | |
Db   173 diyegstivlnelnwtsalddvfknreedpsllwqvfgsatglaryypaspwvndsrtp 232

Qy   269 KKIDLYDVRRRPWYIQGASSPKDMV IIVDVSGSVSGLTLKLMKTSVCEMLDTLSDDDYVN 328
      ||||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db   233 nkidlydvrrrpwyiqgaaspkdmlilvdvsgsvsgltklirtsvssemletlsdddfvn 292

Qy   329 VASFNEKAQPVSCFTHLVQANVRNKKVFKEAVQGMVAKGTTGYKAGFEYAFDQLQNSNIT 388
      |||| | | ||| ||||| |:| | :| | | | | |:| | | |:|
Db   293 vasfnsnaqdvscfqhlvganvrnkvlkdavnnitakgitdykkgfsfafeqllnynvs 352

Qy   389 RANCNKMMFTDGGEDRVQDVFEKYNWPNRTVRVFTFSVGQHNVDVTPLQWMACANKGY 448
      ||||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db   353 rancnkiimlftdggeeraqeifakyn-kdkkvrvftfsvgqhnydrqpiqwmacenkg 411

Qy   449 YFEIPSIGAIRINTQEYLDVLRPMVLGKQVQWTVNVEDALGLGLVVTGTLPVFNL 508
      |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db   412 yyeipsigairintqeyldvlgpvmvlagdkakqvqwtvnyldalelglvitgtlpvfni 471

Qy   509 TQ--DGPGEKKQLILGVMGIDVALNDIKRLTPNYTLGANGYVFAIDLNGYVLLHPNLKP 566
      | :| | | | | | |:| | | | | | |:| | | | | | |:| | | | | |
Db   472 tgqfenktnlknqlilgvmgvdvsledikrltprftlcpngyyfaidpngyvllhpnlpq 531

Qy   567 Q-----TTNFR-----EPVTLDFLDAELEENKKEEIRSMIDGNKGHKQIR 607
      : | | | | | | | |:| | | | | | |:| | | | | | |:| | | | | |
Db   532 kpigvgiptinlrkrpvnqnpksqepvtldfldaelendikveirnkmidgesgektfr 591

Qy   608 TLVKS LDERYIDEVTRNYTWVPIRSTNY-SLGLVLPPYSTFYLQANLSDQILQVKYFEFL 666
      |||| | | | |:| | | |:| | | | |:| | | | |:| | | | |:| | | |
Db   592 tlvksqderyidkgnrtytwtvpngtdysslalvlpptysfyyikakieetitqarysetl 651

```

Qy 667 LPSSFEGHVFIAPREYCKDLNASDNNTEFLKNFIELMEKVTPDSKQCNNFLLHNLILD 726  
 | :|| | : || | :|| | | | | | | | | | : : | : : | | : : : ||  
 Db 652 kpdnfeesgytflaqrDYcsdlkpsdnntefllnfnefidrktpnngscntdlinrvlld 711  
  
 Qy 727 TGITQQLVERVWRDQDLNTYSLLAVFAATDGGITRVFPNKAEDWTENPEPFNASFYRRS 786  
 | | : || : | | | : | | | | | | | | : | : | | | | : | | : ||  
 Db 712 agftnelvqnywskqk-nikgvkarfvvtdggitrvykpeagenwqenpetyedsfykrs 770  
  
 Qy 787 LDNHGYVFKPPHQDALLRPLELENDTVGILVSTAVELSLGRRTLRLPAVVGKLDLEAWAE 846  
 ||| ||| | : : | | | : | | | | | | | | : : | : | | | | : | : |  
 Db 771 ldndnyvftapyfnk-sgpgayes---gimvskaveiyiqgkllkpavvgikidvnswie 826  
  
 Qy 847 KFKVLASNRTHQDQPKC-GPNSHCEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQWDQVG 905  
 | : | : | | | | | | | | | | | | | | | | | | | | : | : |  
 Db 827 nf-----tktsirdp--cagp----vcdckrnsdvmcdcvilddggfllmanhddytngiq 875  
  
 Qy 906 RFFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFPVPTVADFLNLAW 965  
 ||| | : | : | | | | : | | | | | | | | | | | | | | | : | : |  
 Db 876 rffgeidpslmlrlvnisvyafnksydyqsvcepgaapkgaghrsayvpsiadilqigw 935  
  
 Qy 966 WTSAAAWSLFQQLLYGLIYHSWFQ-ADPAEAEAGSPETRESSCVMKQTQYYFGSVNASYNA 1024  
 | : ||||| : || | | : : | | : : : | : | : ||||| : | : | :  
 Db 936 wataaawsilqqfllsltfprlleaadmedddftasmskqsciteqtqyffndsksfsg 995  
  
 Qy 1025 IIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPADGPEQCELVQRP 1084  
 : : ||||| : || : || | | : | : | : | : | : | : | : | : | : | :  
 Db 996 vldcgncsrifhveklmntnlifimveskgtpcdtrlligaeq--tsdgpdpdcmvkgp 1053  
  
 Qy 1085 RYRRGPHICFDYNATEDTSDCGRGASFPPSLGLVLSLQLLLL 1126  
 ||| : || : ||| | | : ||| : | | | : : | : ||  
 Db 1054 ryrkpgpdcfdnnvledytdcgvgslnpslwsiiqiqfvll 1095

RESULT 15

W37879

ID W37879 standard; Protein; 1091 AA.

XX

AC W37879;

XX

DT 28-AUG-1998 (first entry)

XX

DE Human calcium channel a2d subunit.

XX

KW Calcium channel; human; central nervous system disorder;

KW Lambert-Eaton syndrome; diagnosis; therapy.

XX

OS Homo sapiens.

XX

PN WO9811131-A2.

XX

PD 19-MAR-1998.

XX

PF 11-SEP-1997; 97WO-US16146.

XX

PR 16-SEP-1996; 96US-0713118.

XX

PA (AMHP ) AMERICAN HOME PROD CORP.

XX

PI Chen ARS, Franco R, Shuey DJ;

XX

DR WPI; 1998-207325/18.

DR N-PSDB; V29060.

XX

PT DNA encoding human neuronal calcium channel subunit(s) - useful for  
 PT diagnosis of and treatment of central nervous system disorders, e.g.  
 PT Lambert-Eaton syndrome

```

XX
PS Disclosure; Fig 2; 89pp; English.
XX
CC This polypeptide comprises the a2d subunit of the human neuronal
CC calcium channel. cDNA clones (see V29059-61) encoding the a1B
CC subunit (see W37878), the a2d subunit and a b3 subunit (see W37880)
CC have been isolated. These have been inserted into expression
CC vectors and are stably expressed in transformed cell lines. The
CC transformed cells show omega-conotoxin GVIA binding activity,
CC and omega-conotoxin GVIA toxin sensitive potassium-stimulated
CC calcium upstroke, indicating that the proteins expressed by the
CC clones are capable of forming a functioning calcium channel.
CC Nucleic acids encoding the 3 subunits, as well as vectors, host
CC cells and methods of isolating nucleic acids encoding related
CC calcium channels are disclosed. Fusion proteins incorporating the
CC subunit proteins, antibodies, and assays for identifying agents
CC that modulate calcium channel activity are also provided. Such
CC agents can be used to treat certain central nervous system
CC disorders by altering calcium channel activity. Methods of
CC diagnosing diseases associated with particular calcium channels,
CC such as Lambert-Eaton syndrome, are disclosed.
XX
SQ Sequence 1091 AA;

Query Match 49.8%; Score 3030.5; DB 19; Length 1091;
Best Local Similarity 53.8%; Pred. No. 6.1e-258;
Matches 591; Conservative 175; Mismatches 293; Indels 39; Gaps 15;

Qy 44 LWLLLPLLLAAPGASAYSFPQOHTMQHWARRLEQEV DGV MRIFGGVQQLREIYKDNRN 103
| | | | | : | | | | : : : : : : : | | | : | : :
Db 7 laltltlfqsligpsseepfpsavtikswvdkmqedlvltaktasgvnqlvdiyekyqd 66

Qy 104 LFEVQENEPQKLVEKVAGDIESLLDRKVQALKRLADAAENFQKAHRWQDNIKEEDIVYYD 163
| : | : | : : | | | | | | | : : | | | | | | | : : : : : : : : : | :
Db 67 lytvepnnaqlveiaardiekllsnrskalvslaleakvqaahqwredfasnevvyyn 126

Qy 164 AKADAELDDPESEDVERGSKASTLRLDFIEDPNFKNKVNYSYAAVQIPTDIYKGSTVILN 223
| | | | | | | | | | | : : : | | | | | : : | | | | | : : : |
Db 127 akddl---dpekndsepgs--rikpvfiedanfgqrqisyqhaavhiptdiyegstivln 181

Qy 224 ELNWTEALENVFMENRRQDPTLLWQVFGSATGVTRYYPATPW---RAPKKIDLYDVRRR 279
| | | | | | | | | | | : | | : | : | : | : | : | : | : | : | : | : |
Db 182 elnwtasaldevfkknreedpsllwqvfgsatglaryypaspwvdsnrtpnkidlydvrrr 241

Qy 280 PWYIQGASSPKDMVIVDVSGSVSGLTLKLMKTSVCEMLDTLSDDDYVNVASFNEKAQPV 339
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 242 pwyiqgaaspkdmliilvdvsgsvsgltklirtsvsemletlsdddfvnvasfnsnaqdv 301

Qy 340 SCFTHLVQANVRNKKVFKEAVQGMVAKGTTGYKAGFEYAFDQLQNSNITRANCNKMIMMF 399
| | | | | | | | | | | : | : | : | | | | | : : | : | : | : | : |
Db 302 scfqhlvganvrnkvlkdavnnitakgitdykkgfsfafeqllnynvsrancnkiimlf 361

Qy 400 TDGGEDRVQDVFEKYNWPNRTVRVFTFSVGQHNYDVTPLQWMACANKGYGYFEIPSIGAIR 459
| | | | : | : | | | : : | | | | | : | : | | | | | : | : | : | : |
Db 362 tdggeeraqeifnkyn-kdkkvrvfrfsvgqhnyergpiqwmacenkgyyeipsigair 420

Qy 460 INTQEYLDVLRPMVLGKQVQWNTNVYEDALGLGLVVTGTLPVFNLTQ--DGPGEKK 517
| | | | | | | | | | | : | | | | | | | | | | | : | : | : | : |
Db 421 intqeyldvlgpmvlagdkakqvqwtvnyldalelglvitgtlvpfnitgqfenktnlk 480

Qy 518 NQLILGVMGIDVALNDIKRLTPNYTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVT 577
| | | | | : | : | | | | | : | | | | | | | | | | : | : | : | : |
Db 481 nqlilgvmgvdvsledikrltprftlcpngyyfaidpngyallhpnlpknpksqepvtl 540

Qy 578 DFLDAELEDENKEEIRSMIDGNKGHKQIRTLVKS LDERYIDEVTRNYTWVPIRSTNYS 637
| | | | : | | | | | | | | | | | : | | | | | : | | | : | : |
Db 541 dflaelendikveirnmidgesgektftrlvksqderydkgnrtytwtpvngtdysl 600

Qy 638 GLVLPPYSTFY LQANLSDQILQ-----VKYFEFLPSSFESEGHVFIAPREYCKDLNA 690
| | | | | : | : | | | : | | | : | : | : | : | : |

```





Db 481 NQLILGVMGVDVSLEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPKNPKSQEPVTL 540  
 Qy 578 DFLDAELEDENKEEIRRMIDGNKGHKQIRTLVKSLDERVIDEVRNYTWVPIRSTNYSL 637  
 Db 541 DFLDAELEDENKEEIRRMIDGNKGHKQIRTLVKSLDERVIDEVRNYTWVPIRSTNYSL 600  
 Qy 638 GLVLPPYSTFYQLQANLSDQILQVKYFEFLLPSSFESEGHVFIAPREYCKDLNASDNNTEF 697  
 Db 601 ALVLPYTFYIKAKLEETITQARYSETLKPDPNFEESEGYTFIAPRDYCNLKDSDNNTEF 660  
 Qy 698 LKNFIELMEKVTDPKQCNFLHNLILDTGITQQLVERVWRDQDLNTYSLAVFAATDG 757  
 Db 661 LLNFNEFIDRKTPNNPSCNADLINRVLLDAGFTNELVQNYWSKQK-NIKGVKARFVVDG 719  
 Qy 758 GITRVFPNKAEDWTENPEPFNASFYRRSLDNHGYVFKPPHQDALLRPLELENDTVGILV 817  
 Db 720 GITRVYPKEAGENWQENPETYEDSFYKRSNDNDNYVFTAPYFNK-SGPGAYES---GIMV 775  
 Qy 818 STAVELSLGRRTLPAVVGKLDLEAWAEKFKVLASNRTHQDQPKC-GPNSHCEMDCEV 876  
 Db 776 SKAVEIYIQGKLLKPAVVGKIDVNSWIENF-----TKTSIRDP--CAGP----VCDCKR 824  
 Qy 877 NNEDLLCVLIDDGGFLVLSNQHWDQVGRFFSEVDANLMLALYNNSFYTRKESYDYQAA 936  
 Db 825 NSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYAFNKSYDYQSV 884  
 Qy 937 CAPQPPGNLGAAPRGVFPVTVADFLNLAWWTSAAAWSLFQQLLYGLIYHSWFQADPAEAE 996  
 Db 885 CEPGAAPKQGAGHRSAVPSVADILQIGWWATAAAWSILQQFLSLTFPRLLEAVEMEDD 944  
 Qy 997 G-SPETRESSCVMKQTQYFFGSVNASYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLC 1055  
 Db 945 DFTASLSKQSCITEQTQYFFDNDSKSFSGVLDGNCNCRIFHGEKLMNTNLFIMVESKGT 1004  
 Qy 1056 SQCEAGRLLQKETHCPADGPEQCELVQRPRYRRGPHICFDYNATEDTSDCGRGASFPPSL 1115  
 Db 1005 CPCDTRLLIQAEQ--TSDGPNPCDMVKQPRYRKGPVCFDNNVLEDYTDCCGGVSGLNPSL 1062  
 Qy 1116 GVLVSLQLLLL 1126  
 Db 1063 WYIIGIQFLLL 1073

GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 15, 2001, 13:19:43 ; Search time 392.32 Seconds  
 (without alignments)  
 426.713 Million cell updates/sec

Title: US-09-397-550-20  
 Perfect score: 6089  
 Sequence: 1 MAVPARTCGASRPGPARTAR.....LLGLPPRPQPQVLVHASRRL 1145

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 901707 seqs, 146207799 residues

Total number of hits satisfying chosen parameters: 901707

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries